

Full-scale agricultural biogas plant metal content and process parameters in relation to bacterial and archaeal microbial communities over 2.5 year span

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Introduction

Anaerobic digestion is an important source of renewable electrical and thermal energy from various types of organic waste. Biogas can in addition provide a source of biomethane that can be injected into the existing natural gas system. Anaerobic digestion is driven by complex microbial community of archaea and bacteria. The aim of this study was to improve the understanding of community dynamics in context with physico-chemical parameter. For this purpose we followed a 4 MW biogas plant in Vučja vas from the start-up in 2011 to 2014. The biogas plant is composed of 6 digester and 2 post-digesters with a total volume of 34,286 m³.

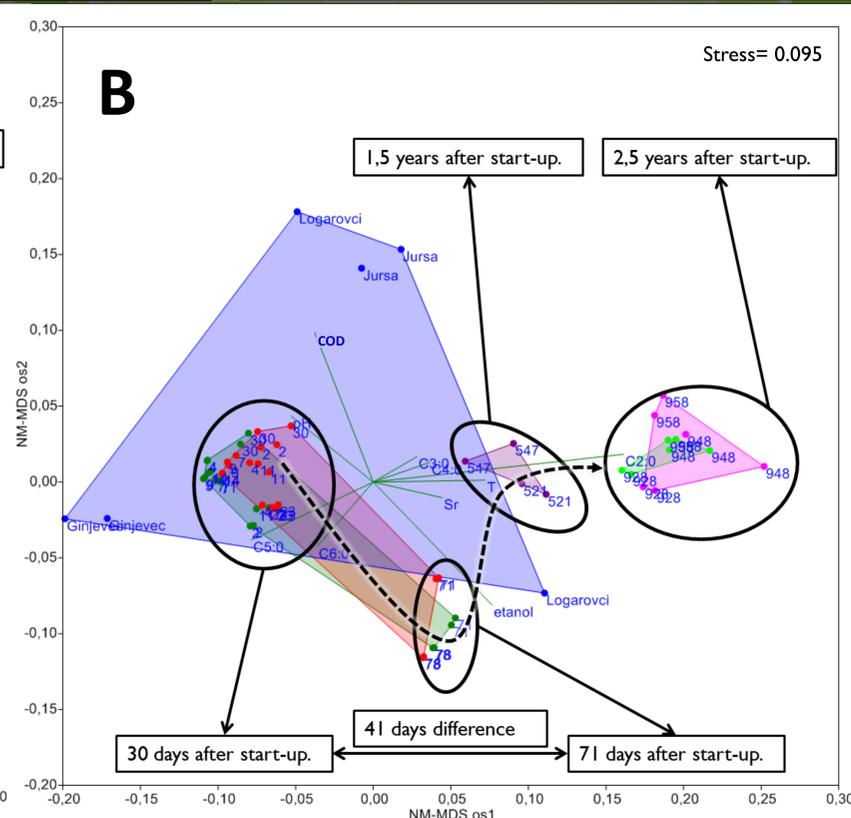
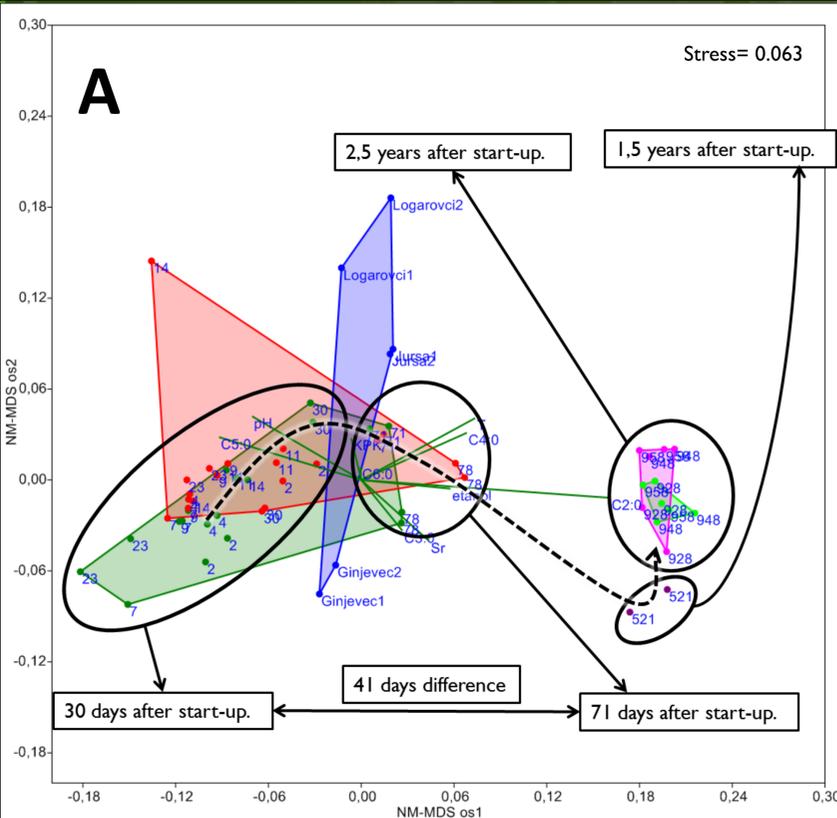
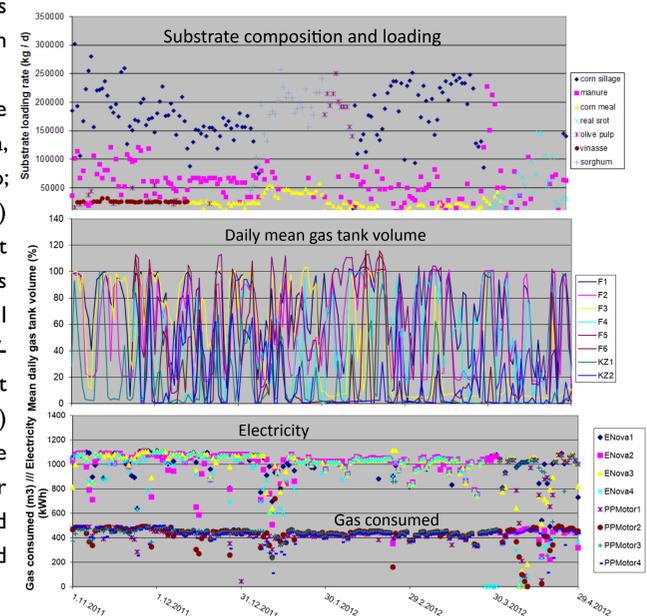


Image 1: Biogas plant Vučja vas

Materials and methods

A three-week start-up was accomplished by daily input from three donor digesters.

Samples were taken from (i) the three donor digesters (Logarovci, Jurša, Ginjevec) at the time of the start-up; (ii) from two serial digesters (F1, F2) at all timepoints (n=13); (iii) and at one timepoint from all six digesters (F1 – F6). Physico-chemical parameters (T°, pH, COD, TSOC UV-VIS absorption spectra, SCFA content and composition, XRF metal profile) and microbial community structure (16S rRNA gene fast molecular profiling with T-RFLP) were assessed and compared to BGP electrical and biogas output (see examples to the right).



Results

Image 3: Nonmetric multidimensional scaling of (A) Archaeal and (B) bacterial community profiles with associated (green lines) Physico-chemical parameters. The shown Physico-chemical parameters are Temperature (T), chemical oxygen demand (COD), pH, ethanol, acetate (C2:0), propionate (C3:0), butyrate (C4:0), pentanoate (C5:0), hexanoate (C6:0) and S_r. The used similarity index is Bray-Curtis. The profiles are colored groups as follows: Digester 1, day 2 to 78 (dark green); Digester 1, day 928 to 958 (light green); Digester 2, day 2 to 78 (red); Digester 2, day 521 to 547 (purple); Digester 2, day 928 to 958 (pink); Digesters Ginjevec, Jurša, Logarovci, day 0 (blue).

Conclusions

- Microbial communities remained functionally stable despite the intake of various substrates at various loadings and produced biogas throughout the entire observed time frame. The most variable parameters throughout the monitoring were SCFA.
- Microbial community profiles diverged from those observed in the donor digesters, presumably due to different environmental pressures established within the recipient digesters.
- The changes in microbial communities were more rapid at the start-up phase than later on.
- The bacterial communities clearly separated themselves from the communities of the first month (day 2 to 30) after the first three months (day 78). This separation is less apparent in the Archaeal community profiles. At the same time points there were only minor difference in physio-chemical parameters and the microbial community composition between digesters F1 and F2.
- The parameters most associated with the bacterial community dynamics between various time points was acetate and TSOC. While archaea communities showed the same correlation with acetate, they showed little to no correlation with TSOC.
- Although digesters F1 to F6 have different substrate intake they showed little differences in microbial community and physiochemical parameters at the same time-point, except for SCFA (not shown).
- Variation partitioning was conducted in order to identify the most important parameters associated with changes in microbial communities. The results show that a large fraction of variability in bacterial and archaeal microbial communities (>55%) remained unexplained although the biogas production process was not affected. This shows that additional parameters such as in situ – metal availability would need to be measured, possibly at different scales, in order to fully elucidate the variables responsible for reorganization of microbial communities beyond random noise. The results also show that reorganization of microbial communities is not necessarily directly associated with impact on performance in full scale biogas reactors.

References

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